

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 03:54:43 : Search time 272 Seconds

(without alignments)
1275.028 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggcgagctggctatctc.....gagatgaccagctcgccg 154

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	24	Plasmid pKS133 2X
2	154	100.0	154	24	Plasmid pKS133 2X
3	154	100.0	154	24	Plasmids pKS133 2X
4	154	100.0	154	24	Plasmids pKS133 2X
5	112	72.7	4974	24	Plasmid pKS133 DNA
6	112	72.7	4974	24	Plasmid pKS133 DNA
7	82.8	53.8	6611	24	pBS68 plasmid used
8	82.8	53.8	6611	24	pBS68 plasmid used
9	81	52.6	81	24	Artificial DNA seq

C	10	81	52.6	81	24	ABK10711	Artificial DNA seq
C	11	81	52.6	963	24	AAD29247	Plasmid pBS149 2X
C	12	81	52.6	963	24	AAD29247	Plasmid pBS149 2X
C	13	80	51.9	80	24	AAD32907	Plasmids pKS106, p
C	14	80	51.9	80	24	AAD32907	Plasmids pKS106, p
C	15	80	51.9	80	24	AAD29230	Plasmids pKS106, p
C	16	80	51.9	80	24	AAD29230	Plasmids pKS106, p
C	17	80	51.9	92	24	ABK10712	Artificial DNA seq
C	18	80	51.9	92	24	ABK10712	Artificial DNA seq
C	19	80	51.9	92	24	AAD29232	ELVISLIVES complem
C	20	80	51.9	92	24	AAD29232	ELVISLIVES complem
C	21	45.8	29.7	1717	24	AAD29242	Plasmid pBS68 2X E
C	22	45.8	29.7	1717	24	AAD29242	Plasmid pBS68 2X E
C	23	44	28.6	44	24	ABK10710	Artificial DNA seq
C	24	44	28.6	44	24	ABK10710	Artificial DNA seq
C	25	34.8	22.6	1681	24	AA518438	Contig 115 DNA enc
C	26	34.8	22.6	1681	24	AA518438	Contig 115 DNA enc
C	27	34.6	22.5	1498	23	AA559803	Propionibacterium
C	28	34.6	22.5	1498	23	AA559803	Propionibacterium
C	29	34.6	22.5	6422	23	AA559655	Propionibacterium
C	30	34.6	22.5	6422	23	AA559655	Propionibacterium
C	31	34	22.1	4403765	22	AA199683	Mycobacterium tube
C	32	34	22.1	4411529	22	AA199682	Mycobacterium tube
C	33	34	22.1	4411529	22	AA199682	Mycobacterium tube
C	34	33.8	21.9	2821	22	AA166075	Triticum aestivum
C	35	33.8	21.9	2821	22	AA166075	Triticum aestivum
C	36	33.2	21.6	1575	22	AAF60762	Pseudomonas sp ABC
C	37	33.2	21.6	1575	22	AAF60762	Pseudomonas sp ABC
C	38	33	21.4	345	21	AA04565	Human secreted pro
C	39	33	21.4	345	21	AA04565	Human secreted pro
C	40	32.8	21.3	9210	22	AAH52046	Mycobacterium tube
C	41	32.8	21.3	9210	22	AAH52046	Mycobacterium tube
C	42	32.8	21.3	4403765	22	AA199683	Mycobacterium tube
C	43	32.4	21.0	2237	16	AAQ89779	Cotransporter prot
C	44	32.4	21.0	2237	16	AAQ89779	Cotransporter prot
C	45	32	20.8	2119	20	AAH87902	Human cell cycle r

ALIGNMENTS

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RESULT 1
AAD32908
ID AAD32908 standard; DNA; 154 BP.
XX
AC AAD32908;
XX
XX 01-JUL-2002 (first entry)
XX
DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
XX
KW Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133;
KW gene; ds.
XX
OS Unidentified.
XX
FH Key
FT CDS Location/Qualifiers
FT CDS /tag= a
FT CDS /product= "ELVISLIVES protein"
FT CDS /tag= b
FT CDS /product= "ELVISLIVES protein"
FT CDS /tag= c
FT CDS /product= "ELVISLIVES protein"
FT CDS /tag= d
FT CDS /product= "ELVISLIVES protein"
XX
XX WO200216565-A2.

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PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US26246.
XX
XX 22-AUG-2000; 2000US-226996P.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
PI WPI; 2002-269353/31.
XX P-PSDB; AAE20554.
DR
XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT useful in creating transgenic plants having altered levels of mono-,
PT poly- and unsaturated fatty acids and in increasing the unsaturation
PT levels in cellular lipids
XX
PS Example 9; Page 43; 77pp; English.
XX
CC The present invention relates to diverged delta-9 fatty acid desaturase
CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC sequences may be used to increase the level of unsaturation in cellular
CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC the same or other plant species and to create transgenic plants in which
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found,
CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC those cells. They are useful as probes for genetic and physical gene
CC mapping and as markers, e.g. restriction fragment length polymorphism
CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC antibodies specific for the peptides and proteins. The present sequence
CC is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133
CC This sequence is used in the exemplification of the invention for the
CC suppression of Fad2 in soybean.
XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;

Query Match 100.0%; Score 154; DB 24; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.5e-29;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCGGAGTGGTCACTCGCTCATCTCGAGTCGGCGCGGAGCTGGTCACTCGCT 60
DB 1 CGGCGGAGTGGTCACTCGCTCATCTCGAGTCGGCGCGGAGCTGGTCACTCGCT 60
QY 61 CATCGTCGAGTCGGCGCGCGGCGGAGTGGTCACTCGAGTCGAGTACCGAGTCCGCGCGC 120
DB 61 CATCGTCGAGTCGGCGCGCGGCGGAGTGGTCACTCGAGTCGAGTACCGAGTCCGCGCGC 120
QY 121 ACTCGAGTCGAGTCGAGTACCGAGTCCGCGCGC 154
DB 121 ACTCGAGTCGAGTCGAGTACCGAGTCCGCGCGC 154

RESULT 2

AAD32908/C
ID AAD32908 standard; DNA; 154 BP.

XX
AC AAD32908;

XX
DT 01-JUL-2002 (first entry)

DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.

XX Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133;
KW gene; ds.
XX

OS Unidentified.

XX Key Location/Qualifiers

RESULT 3
AAD29231

FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT 44..74
FT /*tag= b
FT /product= "ELVISLIVES protein"
FT complement (82..111)
FT /*tag= c
FT /product= "ELVISLIVES protein"
FT complement (119..148)
FT /*tag= d
FT /product= "ELVISLIVES protein"
XX

W0200216565-A2.

28-FEB-2002.

22-AUG-2001; 2001WO-US26246.

22-AUG-2000; 2000US-226996P.

(DUPO) DU PONT DE NEMOURS & CO E I.

Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;

WPI; 2002-269353/31.

P-PSDB; AAE20554.

New delta-9 fatty acid desaturase polypeptides and polynucleotides,
useful in creating transgenic plants having altered levels of mono-,
poly- and unsaturated fatty acids and in increasing the unsaturation
levels in cellular lipids

Example 9; Page 43; 77pp; English.

The present invention relates to diverged delta-9 fatty acid desaturase
proteins and polynucleotides encoding such proteins. The nucleic acid
sequences may be used to increase the level of unsaturation in cellular
lipids, including oil, in tissues when the enzyme is absent or rate-
limiting, to isolate cDNAs and genes encoding homologous proteins from
the same or other plant species and to create transgenic plants in which
the polypeptides are present at higher or lower levels than normal or in
cell types or developmental stages in which they are not normally found,
thus altering the level of mono-, poly- and unsaturated fatty acids in
those cells. They are useful as probes for genetic and physical gene
mapping and as markers, e.g. restriction fragment length polymorphism
(RFLP) markers. The peptides can be used to immunise animals to produce
antibodies specific for the peptides and proteins. The present sequence
is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133
This sequence is used in the exemplification of the invention for the
suppression of Fad2 in soybean.

SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;

Query Match 100.0%; Score 154; DB 24; Length 154;

Best Local Similarity 100.0%; Pred. No. 6.5e-29;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGTGGTCACTCGCTCATCTCGAGTCGGCGCGGAGCTGGTCACTCGCT 60
|||||

DB 154 CGGCGGAGTGGTCACTCGCTCATCTCGAGTCGGCGCGGAGCTGGTCACTCGCT 95
|||||

QY 61 CATCGTCGAGTCGGCGCGCGGCGGAGTGGTCACTCGAGTCGAGTACCGAGTCCGCGCGC 120
|||||

DB 94 CATCGTCGAGTCGGCGCGCGGCGGAGTGGTCACTCGAGTACCGAGTCCGCGCGC 35
|||||

QY 121 ACTCGAGTCGAGTCGAGTACCGAGTCCGCGCGC 154
|||||

DB 34 ACTCGAGTCGAGTCGAGTACCGAGTCCGCGCGC 1
|||||

ID AAD29231 standard; DNA; 154 BP.
XX
AC AAD29231;
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
XX
KW Recombinant construct; gene expression; plasmid pKS133; ds.
XX
OS Unidentified.

XX Key Location/Qualifiers
PH FT 7..36
FT CDS /tag= a
FT /product= "ELVISLIVES protein"
FT CDS 44..74
FT /tag= b
FT /product= "ELVISLIVES protein"
FT complement (82..111)
FT /tag= c
FT /product= "ELVISLIVES protein"
FT complement (119..148)
FT /tag= d
FT /product= "ELVISLIVES protein"

XX WO200200904-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US19962.

XX 23-JUN-2000; 2000US-213961P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;

XX WPI: 2002-139927/18.

XX P-PSDB; AAE18333.

XX New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a
PT target mRNA and its reverse complement unrelated to endogenous DNA, for
PT reducing gene expression -

XX Claim 45; Page 37; 77pp; English.

XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 2X ELVISLIVES complementary repeat region
CC DNA found in plasmid pKS133 used in the exemplification of the invention.

XX Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;

XX Query Match 100.0%; Score 154; DB 24; Length 154;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-29;
XX Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCGCCGAGCTGCTATCTCGTCAATCGTCGAGTCGCGCGCGCGAGCTCGCTCGCT 60
DB 1 CGCGCCGAGCTGCTATCTCGTCAATCGTCGAGTCGCGCGCGCGAGCTCGCTCGCT 60

OY 61 CATCGTCGAGTCGCGCGCGCGCGCGCGCGCGAGTCGAGTCGAGTCGCGCGCG 120
DB 61 CATCGTCGAGTCGCGCGCGCGCGCGCGCGCGAGTCGAGTCGAGTCGCGCGCG 120
OY 121 ACTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGCGCGCGCGCGCG 154
DB 121 ACTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGCGCGCGCGCGCG 154

RESULT 4

AAD29231/c

ID AAD29231 standard; DNA; 154 BP.

XX AC AAD29231;

XX DT 07-MAY-2002 (first entry)

XX Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.

XX Recombinant construct; gene expression; plasmid pKS133; ds.

XX Unidentified.

XX Key Location/Qualifiers
PH FT 7..36
FT CDS /tag= a
FT /product= "ELVISLIVES protein"
FT CDS 44..74
FT /tag= b
FT /product= "ELVISLIVES protein"
FT complement (82..111)
FT /tag= c
FT /product= "ELVISLIVES protein"
FT complement (119..148)
FT /tag= d
FT /product= "ELVISLIVES protein"

XX WO200200904-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US19962.

XX 23-JUN-2000; 2000US-213961P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;

XX WPI: 2002-139927/18.

XX P-PSDB; AAE18333.

XX New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a
PT target mRNA and its reverse complement unrelated to endogenous DNA, for
PT reducing gene expression -

XX Claim 45; Page 37; 77pp; English.

XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from

CC It. The present sequence is 2X ELVISLIVES complementary repeat region
CC DNA found in plasmid pKS133 used in the exemplification of the invention.

XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;
XX

Query Match	100.0%	Score 154	DB 24	Length 154
Best Local Similarity	100.0%	Pred. No. 6.5e-29		
Matches 154	Conservative	0	Mismatches 0	Indels 0

1 CGGCCGAGCTGCTCATCTCGCTCATCTCGTGGCGCGGAGCTGTCATCTCGCT 60
 154 CGSCCGAGCTGCTCATCTCGCTCATCTCGTGGCGCGGAGCTGTCATCTCGCT 95

[illegible][illegible]

RESULT 5

Db 34 ACTCGAGATGAGCGAGATGACCGAGCTCGGCGG 1

ABK10072
ID ABK10072 standard; DNA; 4974 BP.
XX
AC ABK10072;

XX
DT 05-JUN-2002 (first entry)
XX
DE Plasmid pKS133 DNA.

XX	
XX	Plastidic phosphoglucomutase; gene; ds; plasmid pKS133.
XX	
OS	Synthetic.

00 07/06/2002
 XX
 PN EPI174510-A2.
 XX
 PD 23-JAN-2002

FD 23 JAN 2002.
XX
XX
PF 17-JUL-2001; 2001EP-0306143.
XX
XX 17-JUN-2000; 2000US-2187129
DP

17-JUL-2000; 2000US-218/12P.
(DUPO) DU PONT DE NEMOURS & CO E I.

PI Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
XX WPI; 2002-156692/21.
XX

PT Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein levels -

XX
PS
XX
CC

CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of

CC cell under conditions that are suitable for expression of the chimeric
 CC gene, where the expression of the gene results in production of altered
 CC levels of plastidic phosphoglucomutase. This sequence represents plasmid
 CC DNA used in the methods of the invention.

CC Note: This sequence is not represented in the printed specification but
 CC is based on sequence information supplied by the European Patent Office.

XX Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 1 other;

Query Match 72.7%; Score 112; DB 24; Length 4974;
 Best Local Similarity 100.0%; Pred. No. 1.3e-18;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 4974 GGAGCTGGTCACTCGCTCATCTCGAGTCGGCGCCGCGACTCGACCATGAGCGAGAT 4915

QY 103 GACCAGCTCCGCCGCCGCGACTCGACCATGAGCGAGATGACCGCTCCGCCCG 154
 |||||
 Db 4914 GACCAGCTCCGCCGCCGCGACTCGACCATGAGCGAGATGACCGCTCCGCCCG 4863

RESULT 7

AAD32909
 ID AAD32909 standard; DNA; 6611 BP.

AC AAD32909;

XX 01-JUL-2002 (first entry)

DE PBS68 plasmid used for diverged delta-9 desaturase suppression.

KW Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
 KW oil; transgenic plant; gene mapping; immunisation; plasmid PBS68; ds.

OS Unidentified.

XX Key Location/Qualifiers

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FT /*tag= b

FT /label= Kit3_terminator

FT complement (880..1920)

FT /*tag= b

FT /note= "Hygromycin selection region"

FT promoter 3260..5348

FT /*tag= c

FT /label= Kit3_promoter

XX WO200216565-A2.

XX 28-FEB-2002.

XX 22-AUG-2001; 2001WO-US26246.

XX 22-AUG-2000; 2000US-226996P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;

XX WPI; 2002-269353/31.

XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
 PT useful in creating transgenic plants having altered levels of mono-,
 PT poly- and unsaturated fatty acids and in increasing the unsaturation
 PT levels in cellular lipids -

XX Example 9; Page 76-77; 77pp; English.

XX The present invention relates to diverged delta-9 fatty acid desaturase
 CC proteins and polynucleotides encoding such proteins. The nucleic acid
 CC sequences may be used to increase the level of unsaturation in cellular
 CC lipids, including oil, in tissues when the enzyme is absent or rate-

CC limiting, to isolate cDNAs and genes encoding homologous proteins from
 CC the same or other plant species and to create transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found,
 CC thus altering the level of mono-, poly- and unsaturated fatty acids in
 CC those cells. They are useful as probes for genetic and physical gene
 CC mapping and as markers, e.g. restriction fragment length polymorphism
 CC (RFLP) markers. The peptides can be used to immunise animals to produce
 CC antibodies specific for the peptides and proteins. The present sequence
 CC is plasmid PBS68 which is used for the suppression of diverged delta-9
 CC desaturase in high stearate phenotypes. This sequence is used in the
 CC exemplification of the invention.

CC Note: The sequence data for this sequence (AAD32909) corresponding to
 CC position 1501 to 6611 is not represented in the printed specification
 CC but is based on the sequence information supplied by the European patent
 CC office.

XX Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 1 other;

Query Match 53.8%; Score 82.8; DB 24; Length 6611;
 Best Local Similarity 97.7%; Pred. No. 1.7e-11;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGCGACTCGCTCGCT 60
 |||||
 Db 5348 CGGCGGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGCGACTCGCTCGCT 5407

QY 61 CATCTCGAGTCGGCGCCGCGCGACT 86

Db 5408 CATCTCGAGTCGGCGCCGCGCGTGTAGT 5433

RESULT 8

AAD32909/c

ID AAD32909 standard; DNA; 6611 BP.

XX AAD32909;

XX 01-JUL-2002 (first entry)

DE PBS68 plasmid used for diverged delta-9 desaturase suppression.

KW Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
 KW oil; transgenic plant; gene mapping; immunisation; plasmid PBS68; ds.

OS Unidentified.

XX Key Location/Qualifiers

FT terminator 523..725

FT /*tag= b

FT /label= Kit3_terminator

FT complement (880..1920)

FT /*tag= b

FT /note= "Hygromycin selection region"

FT promoter 3260..5348

FT /*tag= c

FT /label= Kit3_promoter

XX WO200216565-A2.

XX 28-FEB-2002.

XX 22-AUG-2001; 2001WO-US26246.

XX 22-AUG-2000; 2000US-226996P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;

XX WPI; 2002-269353/31.

XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,

PT useful in creating transgenic plants having altered levels of mono-,
 PT poly- and unsaturated fatty acids and in increasing the unsaturation
 PT levels in cellular lipids
 XX
 PS Example 9; Page 76-77; 77pp; English.
 XX
 CC The present invention relates to diverged delta-9 fatty acid desaturase
 CC proteins and polynucleotides encoding such proteins. The nucleic acid
 CC sequences may be used to increase the level of unsaturation in cellular
 CC lipids, including oil, in tissues when the enzyme is absent or rate-
 CC limiting, to isolate cDNAs and genes encoding homologous proteins from
 CC the same or other plant species and to create transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found,
 CC thus altering the level of mono-, poly- and unsaturated fatty acids in
 CC those cells. They are useful as probes for genetic and physical gene
 CC mapping and as markers, e.g. restriction fragment length polymorphism
 CC (RFLP) markers. The peptides can be used to immunise animals to produce
 CC antibodies specific for the peptides and proteins. The present sequence
 CC is plasmid pBS68 which is used for the suppression of diverged delta-9
 CC desaturase in high stearate phenotypes. This sequence is used in the
 CC exemplification of the invention.
 CC Note: The sequence data for this sequence (AAD32509) corresponding to
 CC position 1501 to 6611 is not represented in the printed specification
 CC but is based on the sequence information supplied by the European patent
 CC office.
 XX

SQ Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 1 other;

Query Match 53.8%; Score 82.8; DB 24; Length 6611;
 Best Local Similarity 97.7%; Pred. No. 1.7e-11;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 69 AGTCGGCGCGCGAGTCGACGATGACGAGATGACGAGTCGCGCGCGACTCGACG 128
 Db 5433 ACTCAGCGCGCGCGAGTCGACGATGACGAGATGACGAGTCGCGCGCGACTCGACG 5374
 QY 129 ATGAGCGAGATGACGAGTCGCGCGCG 154
 Db 5373 ATGAGCGAGATGACGAGTCGCGCGCG 5348

RESULT 9
 ABK10711
 ID ABK10711 standard; DNA; 81 BP.
 XX
 AC ABK10711;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Artificial DNA sequence #3.
 XX
 KW Plastidic phosphoglucumutase; transgenic; plant; gene; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..36
 FT /*tag- a
 FT /product- "ELVISLIVES peptide"
 FT /partial
 FT /note- "No start or stop codon shown"
 FT CDS 44..73
 FT /*tag- b
 FT /product- "ELVISLIVES peptide"
 FT /partial
 FT /note- "No start or stop codon shown"
 XX
 PN EP1174510-A2.
 XX
 PD 23-JAN-2002.
 XX
 PF 17-JUL-2001; 2001EP-0306143.

XX 17-JUL-2000; 2000US-218712P.
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PA Allen SM, Butler KH, Carlson TJ, Ilag LL;
 PI WPI: 2002-156692/21.
 XX P-PSDB; AAU77109.
 DR
 DR Novel isolated polypeptides having phosphoglucumutase activity and
 XX polynucleotides encoding the polypeptides, useful for producing
 PT transgenic plants with altered plastidic phosphoglucumutase protein
 PT levels
 XX
 PS Example 9; Page 19; 27pp; English.
 XX
 CC The invention relates to plastidic phosphoglucumutase polypeptides and
 CC their related nucleic acids. The sequences are useful for producing a
 CC transgenic plant, by transforming a plant cell with a polynucleotide of
 CC the invention and regenerating a plant from the transformed plant cell.
 CC Polynucleotide fragments are useful for suppressing the level of
 CC expression of a gene encoding a polypeptide having plastidic
 CC phosphoglucumutase activity. An isolated polynucleotide that affects the
 CC level of expression of a plastidic phosphoglucumutase polypeptide in a
 CC plant cell can be identified by introducing a DNA fragment comprising at
 CC least 541 nucleotides, measuring the level of the polypeptide in the
 CC plant cell containing the polynucleotide, and comparing the level of the
 CC polypeptide in the plant cell containing the isolated polynucleotide with
 CC the level of the polypeptide in a plant cell that does not contain the
 CC isolated polynucleotide. A method for altering the level of expression of
 CC a plastidic phosphoglucumutase protein in a host cell comprises
 CC transforming a host cell with a chimeric gene and growing the transformed
 CC cell under conditions that are suitable for expression of the chimeric
 CC gene, where the expression of the gene results in production of altered
 CC levels of plastidic phosphoglucumutase. This sequence represents an
 CC artificial DNA used for plasmid construction, in the methods of the
 XX invention.
 SQ Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 other;

Query Match 52.6%; Score 81; DB 24; Length 81;
 Best Local Similarity 100.0%; Pred. No. 3.8e-11;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGCCGAGCTGTCATCTGCTCATCTGAGTCGCGCGCGCGAGCTGGTCATCTGCT 60
 Db 1 CGGCCGAGCTGTCATCTGCTCATCTGAGTCGCGCGCGCGAGCTGGTCATCTGCT 60
 QY 61 CATCTGTCGAGTCGCGCGCGCG 81
 Db 61 CATCTGTCGAGTCGCGCGCGCG 81

RESULT 10
 ABK10711/c
 ID ABK10711 standard; DNA; 81 BP.
 XX
 AC ABK10711;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Artificial DNA sequence #3.
 XX
 KW Plastidic phosphoglucumutase; transgenic; plant; gene; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..36
 FT /*tag- a
 FT /product- "ELVISLIVES peptide"
 FT /partial

DE Plasmid pBS149 2x ELVISLIVES complementary region DNA.

XX Recombinant construct; gene expression; late-soybean-embryo promoter;

KW LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.

KW Unidentified.

OS WO200200904-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US19962.

XX 23-JUN-2000; 2000US-213961P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA (PION-) PIONEER HI-BRED INT INC.

XX Glassman KP, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;

PI Nichols SE;

XX WPI; 2002-139927/18.

XX New recombinant construct having a promoter operably linked to a DNA

PT sequence which when expressed produces an RNA having homology to a

PT target mRNA and its reverse complement unrelated to endogenous DNA, for

PT reducing gene expression -

XX Example 10; Page 72; 77pp; English.

XX The present invention relates to a new recombinant construct. The

CC construct comprises a promoter operably linked to a DNA sequence which

CC when expressed by a host produces an RNA having homology to at least one

CC target mRNA expressed by the host and complementary RNA regions. The

CC recombinant construct is useful for reducing the expression of a target

CC mRNA or any similar endogenous mRNA. The RNAs expressed from the

CC recombinant constructs are also used in reducing expression of a target

CC mRNA or any similar endogenous mRNA. The sequences and their reverse

CC complements can be used to reduce the expression of any endogenous

CC genomic sequence that shares substantial similarity to nucleic acid

CC fragment which is in proximity to the DNA or RNA sequence derived from

CC it. The present sequence is 2x ELVISLIVES complementary region from

CC pBS149 that contains fragments from two soybean galactinol synthase genes

CC GAS1 and GAS2. The region is functionally attached to a late-soybean-

CC embryo promoter (LEA) and a phaseolin 3' terminator region. This

CC entire region is then cloned into BamHI site of pKS136, which contains a

CC 2x ELVISLIVES complementary region controlled by a soybean Kti promoter

CC and terminator region used in the exemplification of the invention.

XX Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 other;

SQ

Query Match 52.6%; Score 81; DB 24; Length 963;

Best Local Similarity 100.0%; Pred. No. 4.3e-11;

Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGAGCTGGTCATCTCGTCATCTCGAGTCGGCGCGGCGGAGCTGGTCATCTCGCT 60

DB 963 CGCGCGGAGCTGGTCATCTCGTCATCTCGAGTCGGCGCGGCGGAGCTGGTCATCTCGCT 904

QY 61 CATCTGTCGAGTCGGCGGCGGCGG 81

DB 903 CATCTGTCGAGTCGGCGGCGGCGG 883

RESULT 13

AAD32907

ID AAD32907 standard; DNA; 80 BP.

XX AAD32907;

AC

XX 01-JUL-2002 (first entry)

DT

XX Plasmids pKS106, pKS124 1x ELVISLIVES complementary repeat DNA.

DE

XX Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;

KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS124;

KW plasmid pKS106; gene; ds.

XX Unidentified.

OS

XX Location/Qualifiers

XX 7..36

PH CDS

FT /*tag= a

FT /product= "ELVISLIVES protein"

FT complement (45..74)

FT /*tag= b

FT /product= "ELVISLIVES protein"

XX WO200216565-A2.

XX 28-FEB-2002.

XX 22-AUG-2001; 2001WO-US26246.

XX 22-AUG-2000; 2000US-226996P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;

PI P-PSDB; AAE20554.

XX WPI; 2002-269353/31.

XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,

PT useful in creating transgenic plants having altered levels of mono-,

PT poly- and unsaturated fatty acids and in increasing the unsaturation

PT levels in cellular lipids -

XX Example 9; Page 43; 77pp; English.

XX The present invention relates to diverged delta-9 fatty acid desaturase

CC proteins and polynucleotides encoding such proteins. The nucleic acid

CC sequences may be used to increase the level of unsaturation in cellular

CC lipids, including oil, in tissues when the enzyme is absent or rate-

CC limiting, to isolate cDNAs and genes encoding homologous proteins from

CC the same or other plant species and to create transgenic plants in which

CC the polypeptides are present at higher or lower levels than normal or in

CC cell types or developmental stages in which they are not normally found,

CC thus altering the level of mono-, poly- and unsaturated fatty acids in

CC those cells. They are useful as probes for genetic and physical gene

CC mapping and as markers, e.g. restriction fragment length polymorphism

CC (RFLP) markers. The peptides can be used to immunise animals to produce

CC antibodies specific for the peptides and proteins. The present sequence

CC is 1x ELVISLIVES complementary repeat region DNA found in plasmids pKS106

CC and pKS124. This sequence is used in the exemplification of the invention

CC for the suppression of Fad2 in soybean.

XX Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 other;

SQ

Query Match 51.9%; Score 80; DB 24; Length 80;

Best Local Similarity 100.0%; Pred. No. 6.7e-11;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGCGCGGAGCTGGTCATCTCGTCATCTCGAGTCGGCGCGGCGGAGCTGGTCATCTCGCT 117

DB 1 CGCGCGGAGCTGGTCATCTCGTCATCTCGAGTCGGCGCGGCGGAGCTGGTCATCTCGCT 80

QY 98 GAGATGACGAGCTCGGCGG 117

DB 61 GAGATGACGAGCTCGGCGG 80

RESULT 14

AAD32907/c

ID AAD32907 standard; DNA; 80 BP.

XX

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AC AAD32907;
XX
XX 01-JUL-2002 (first entry)
XX
XX Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
DE
XX Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS124;
KW plasmid pKS106; gene; ds.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT complement (45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"
XX
XX WO200216565-A2.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US26246.
XX
XX 22-AUG-2000; 2000US-226996P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Booth JR, Caboon RE, Hitz WD, Kinney AJ, Yadav NS;
PI
XX WPI; 2002-269353/31.
DR
XX P-PSDB; AAE20554.
XX
XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT useful in creating transgenic plants having altered levels of mono-,
PT poly- and unsaturated fatty acids and in increasing the unsaturation
PT levels in cellular lipids
XX
XX Example 9; Page 43; 77pp; English.
XX
XX The present invention relates to diverged delta-9 fatty acid desaturase
CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC sequences may be used to increase the level of unsaturation in cellular
CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC the same or other plant species and to create transgenic plants in which
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found,
CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC those cells. They are useful as probes for genetic and physical gene
CC mapping and as markers, e.g. restriction fragment length polymorphism
CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC antibodies specific for the peptides and proteins. The present sequence
CC is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106
CC and pKS124. This sequence is used in the exemplification of the invention
CC for the suppression of Fad2 in soybean.
XX
XX Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 other;
SQ
Query Match 51.9%; Score 80; DB 24; Length 80;
Best Local Similarity 100.0%; Pred. NO. 6.7e-11;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGGTCACTCGCTCATCGTCGAGTCGGCGGCCCGCCGACTCGAGATGAGC 97
DB 80 CGGCCGAGCTGGTCACTCGCTCATCGTCGAGTCGGCGGCCCGCCGACTCGAGATGAGC 21
QY 98 GAGATGACCACTCCGCGCCG 117
DB 20 GAGATGACCACTCCGCGCCG 1
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RESULT 15
AAD29230
ID AAD29230 Standard; DNA; 80 BP.
XX
XX AAD29230;
AC
XX 07-MAY-2002 (first entry)
XX
XX Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
DE
XX Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
KW ds.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT complement (45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"
XX
XX WO200200904-A2.
XX
XX 03-JAN-2002.
XX
XX 22-JUN-2001; 2001WO-US19962.
XX
XX 23-JUN-2000; 2000US-213961P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA
XX P-PSDB; AAE18333.
XX
XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
XX WPI; 2002-139927/18.
DR
XX P-PSDB; AAE18333.
XX
XX New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a
PT target mRNA and its reverse complement unrelated to endogenous DNA, for
PT reducing gene expression
XX
XX Claim 45; Page 37; 77pp; English.
XX
XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region
CC DNA found in plasmids pKS106 and pKS124 used in the exemplification of
CC the invention.
XX
XX Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 other;
SQ
Query Match 51.9%; Score 80; DB 24; Length 80;
Best Local Similarity 100.0%; Pred. NO. 6.7e-11;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGGTCACTCGCTCATCGTCGAGTCGGCGGCCCGCCGACTCGAGATGAGC 97
DB 1 CGGCCGAGCTGGTCACTCGCTCATCGTCGAGTCGGCGGCCCGCCGACTCGAGATGAGC 60
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QY 98 GAGATGACCAGCTCCGCCG 117
|||||
Db 61 GAGATGACCAGCTCCGCCG 80

Search completed: November 19, 2002, 05:24:32
Job time : 302 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	34.8	22.6	1681	4	US-09-434-288-7	Sequence 7, Appli
2	34.8	22.6	1681	4	US-09-434-288-7	Sequence 7, Appli
3	34	22.1	4403765	4	US-09-103-840A-2	Sequence 2, Appl
4	34	22.1	4411529	4	US-09-103-840A-1	Sequence 1, Appl
5	34	22.1	4411529	4	US-09-103-840A-1	Sequence 1, Appl
6	32.8	21.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl
7	32.4	21.0	2238	1	US-07-841-651-1	Sequence 1, Appli
8	32.4	21.0	2238	1	US-07-841-651-1	Sequence 1, Appli
9	32	20.8	2119	3	US-09-032-372-6	Sequence 6, Appli
10	32	20.8	2119	3	US-09-032-372-6	Sequence 6, Appli
11	30.8	20.0	2787	4	US-09-105-537-40	Sequence 40, Appl
12	30.8	20.0	2787	4	US-09-105-537-40	Sequence 40, Appl
13	30.8	20.0	5970	3	US-09-320-878-21	Sequence 21, Appl
14	30.8	20.0	5970	3	US-09-320-878-21	Sequence 21, Appl
15	30.6	19.9	1734	6	5352575-8	Patent No. 5352575
16	30.6	19.9	1734	6	5352575-8	Patent No. 5352575
17	30.4	19.7	11219	3	US-07-642-734C-1	Sequence 1, Appli
18	30.4	19.7	11219	3	US-07-642-734C-1	Sequence 1, Appli
19	30.4	19.7	11219	3	US-08-439-009A-1	Sequence 1, Appli
20	30.4	19.7	11219	3	US-08-439-009A-1	Sequence 1, Appli
21	30.2	19.6	7898	4	US-08-984-709A-49	Sequence 49, Appl
22	30.2	19.6	7898	4	US-08-984-709A-49	Sequence 49, Appl
23	29.8	19.4	3252	2	US-08-809-740A-1	Sequence 1, Appli
24	29.8	19.4	3252	2	US-08-809-740A-1	Sequence 1, Appli
25	29.8	19.4	3252	2	US-08-809-740A-1	Sequence 1, Appli
26	29.8	19.4	3252	2	US-08-809-740A-4	Sequence 4, Appli
27	29.4	19.1	6822	4	US-09-426-998-3	Sequence 3, Appli

Db 747 AGCCGGGTCTCGACACGTC 726
| | | | | | | | | | | | | | | |

RESULT 9

US-09-032-372-6
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
US-09-032-372-6

Query Match 20.8%; Score 32; DB 3; Length 2119;

Best Local Similarity 51.4%; Pred. No. 6.4;

Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 5 CGGAGTGGTCACTCGCTCATCGTGGCGGCGGAGCTGGTCTCGCTCATC 64
| | | | | | | | | | | | | | | |
Db 151 CGAGGTCTCCGCTTCCTCGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 210
| | | | | | | | | | | | | | | |
QY 65 GTGAGTGGCGGCGGCGGAGTGGCGGCGGAGTGGCGGCGGAGTGGCGG 124
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Db 211 CACGAGACGAGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 270
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QY 125 GACGATGAGCGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGT 148
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Db 271 GAGGAGGAGCGGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 294
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RESULT 10

US-09-105-537-40
; Sequence 40, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.

US-09-032-372-6/c
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
US-09-032-372-6

Query Match 20.8%; Score 32; DB 3; Length 2119;

Best Local Similarity 51.4%; Pred. No. 6.4;

Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 7 GAGCTGGTCACTCGCTCATCGTGGCGGCGGAGCTGGTCTCGCTCATCGT 66
| | | | | | | | | | | | | | | |
Db 294 GTGAGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 235
| | | | | | | | | | | | | | | |
QY 67 GAGTGGCGGCGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 126
| | | | | | | | | | | | | | | |
Db 234 CGAGCGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 175
| | | | | | | | | | | | | | | |
QY 127 CGATGAGCGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGG 150
| | | | | | | | | | | | | | | |
Db 174 CGGAGAGGGAAGCGGAGAGCTCG 151
| | | | | | | | | | | | | | | |

RESULT 11

US-09-105-537-40
; Sequence 40, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.

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; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 5970
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21

Query Match 20.0%; Score 30.8; DB 3; Length 5970;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY 57 CGCTCATCGTCGAGTGGCGGCCGCCGACTCGAGATGAGCGGAGATGACCGAGTCCGGCC 116
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2815 CGCTTACTACGTCGTCGCGACCGCGCGGACGCGGAGACCCCGCTCTGCTCG 2874.
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 117 GCGGACTCGACGATGAGCGGAGATCACCAGTCTCCGGCGC 154
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2875 GCGGCTGGCGCGGACGCGGAGACCCCGCTCTGCTCG 2912
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-320-878-21/c
; Sequence 21, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 5970
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21

Query Match 20.0%; Score 30.8; DB 3; Length 5970;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 04:53:30 ; Search time 29 Seconds
(without alignments)
2011.188 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggccgagctggtatctc.....gagatgaccagctcggcgcg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues
Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	72.7	4974	9	US-09-906-209-17
2	112	72.7	4974	9	US-09-906-209-17
3	32.8	21.3	9210	9	US-09-712-363-100
4	32.8	21.3	9210	9	US-09-712-363-100
5	31.8	20.6	1573	10	US-09-822-830A-20
6	31.8	20.6	1573	10	US-09-822-830A-20
7	31.6	20.5	2451	10	US-09-815-242-7752
8	31.6	20.5	2451	10	US-09-815-242-7752
9	31.4	20.4	3202	10	US-09-954-456-210
10	31.4	20.4	3202	10	US-09-954-456-210
11	30.8	20.0	2787	9	US-09-860-846-40
12	30.8	20.0	2787	9	US-09-860-846-40
13	30.8	20.0	2787	10	US-09-861-289-40
14	30.8	20.0	2787	10	US-09-861-289-40
15	30.6	19.9	276	10	US-09-878-574-12270
16	30.6	19.9	276	10	US-09-878-574-12270
17	30.2	19.6	1533	9	US-09-712-363-81
18	30.2	19.6	1533	9	US-09-712-363-81
19	30	19.5	1536	10	US-09-815-242-4092

c	20	30	19.5	1536	10	US-09-815-242-4092	Sequence 4092, Ap
c	21	30	19.5	2280	10	US-09-822-830A-93	Sequence 93, Appl
c	22	30	19.5	2280	10	US-09-822-830A-93	Sequence 93, Appl
c	23	29.8	19.4	427	10	US-09-764-833-98	Sequence 98, Appl
c	24	29.8	19.4	427	10	US-09-764-833-98	Sequence 98, Appl
c	25	29.6	19.2	281	10	US-09-294-093B-171	Sequence 171, App
c	26	29.6	19.2	281	10	US-09-294-093B-171	Sequence 171, App
c	27	29.6	19.2	1575	9	US-09-712-363-78	Sequence 78, Appl
c	28	29.6	19.2	1575	9	US-09-712-363-78	Sequence 78, Appl
c	29	29.6	19.2	3042	9	US-09-712-363-68	Sequence 68, Appl
c	30	29.6	19.2	3042	9	US-09-712-363-68	Sequence 68, Appl
c	31	29.2	19.0	342	10	US-09-783-590-4679	Sequence 4679, Ap
c	32	29.2	19.0	342	10	US-09-783-590-4679	Sequence 4679, Ap
c	33	29.2	19.0	578	10	US-09-833-790-391	Sequence 391, App
c	34	29.2	19.0	578	10	US-09-833-790-391	Sequence 391, App
c	35	29.2	19.0	1100	10	US-09-867-550-1149	Sequence 1149, Ap
c	36	29.2	19.0	1100	10	US-09-867-550-1149	Sequence 1149, Ap
c	37	29.2	19.0	1610	10	US-09-880-107-2203	Sequence 2203, Ap
c	38	29.2	19.0	1610	10	US-09-880-107-2203	Sequence 2203, Ap
c	39	29.2	19.0	4139	10	US-09-880-107-2279	Sequence 2279, Ap
c	40	29.2	19.0	4139	10	US-09-880-107-2279	Sequence 2279, Ap
c	41	29	18.8	1066	9	US-09-764-868-390	Sequence 390, App
c	42	29	18.8	1066	9	US-09-764-868-390	Sequence 390, App
c	43	28.8	18.7	322	10	US-09-867-550-87	Sequence 87, Appl
c	44	28.8	18.7	322	10	US-09-867-550-87	Sequence 87, Appl
c	45	28.6	18.6	88421	9	US-09-976-059-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-906-209-17
; Sequence 17, Application US/09906209
; Patent No. US20020165385A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; APPLICANT: Carlson, Tom
; APPLICANT: Ilag, Lawrence L.
; TITLE OF INVENTION: Plasmidic Phosphoglucosyltransferase Genes
; FILE REFERENCE: BB1451 NA
; CURRENT APPLICATION NUMBER: US/09/906,209
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,712
; PRIOR FILING DATE: JULY 17, 2000
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17:
; LENGTH: 4974
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

Query Match 72.7%; Score 112; DB 9; Length 4974;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGGTCTCATCTCGCTCATCTCGCTCGGCGGCGGAGCTGCTCATCTCGCT 60
DB 4863 CGGCCGAGCTGGTCTCATCTCGCTCATCTCGCTCGGCGGCGGAGCTGCTCATCTCGCT 4922
QY 61 CATCTCGAGTCGGCGGCGGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 112
DB 4923 CATCTCGAGTCGGCGGCGGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 4974
RESULT 2
US-09-906-209-17/c


```

; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-830A-20

Query Match      20.6%; Score 31.8; DB 10; Length 1573;
Best Local Similarity 54.8%; Pred. No. 1.7;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 37 GCGGCGGAGCTGTCATCTCGTCTATCTGTCGAGTCGGCGCGGCGGAGCTCGAGATGAG 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 GCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 97 CGAGATCACCAGCTCCGCGCGGCGGAGCTCGAGATGAGCGAGATGAGCGAGCTCCGG 151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 CGCCCGCGATCCCTTCGCCCCCGGAGCTCGGGGACACGCAAGAACTGCCAGCTCGCG 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-09-822-830A-20/c
; Sequence 20, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-830A-20

Query Match      20.6%; Score 31.8; DB 10; Length 1573;
Best Local Similarity 54.8%; pred. No. 1.7;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 4 CCGGAGCTGTCATCTCGTCTATCTCGTCTATCTCGTCTGAGTCGGCGCGGAGCTGTCATCTCGTCTCAT 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 CCGCAGCTGGAGGTCGTCGTGTCCTCCCGAGCTGGGGGGCGGAAGGGATCGCGGGCGGACGG 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 64 CGTCTGAGTCGGCGCGCGCGGAGCTCGAGATGAGCGAGATGAGCGAGTCCGGCGCGC 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 CGCGGAGCGCGCGCGCGCGGAGCTCGAGATGAGCGAGATGAGCGAGTCCGGCGCGC 68
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-09-815-242-7752
; Sequence 7752, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7752
; LENGTH: 2451
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2451)
; US-09-815-242-7752

Query Match      20.5%; Score 31.6; DB 10; Length 2451;
Best Local Similarity 62.8%; Pred. No. 2;
Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 43 GGAGCTGCTATCTCGCTCATCTCGATCGGCGCGCGCGGAGTCGGCGCGCGGAGTCAAGCGAGACGCGAGAT 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1398 GGACAGATCCTGATCAGCACCGCTCGCGCGCGCGCGGAGTCGGCGCGCGGAGTCAAGCGAGACGCGAGAA 1457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 103 GACCAGCTCGCGCGCGCG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1458 GGCCATCTCGCGCTGCAG 1475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-815-242-7752/c
; Sequence 7752, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

RESULT 9
US-09-954-456-210
Sequence 210, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIORITY APPLICATION NUMBER: US/60/233,617
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: US/60/234,052
PRIORITY FILING DATE: 2000-09-20
PRIORITY APPLICATION NUMBER: US/60/234,923
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,134
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,637
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,638
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,711
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,720
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,840
PRIORITY FILING DATE: 2000-09-27

	Query Match	20.4%	Score 31.4;	DB 10;	Length 3202;
	Best Local Similarity	64.4%	Pred. No. 2.3;		
	Matches	47;	Conservative	0;	Mismatches 26;
					Indels 0;
					Gaps 0;
Qy	48	TGGTCATCTCGCTCATCGTCGAGTCGGGGGGCCGGCGACTCGACCATGAGCGAGATGACCA	107		
Db	1566	TGGGGCTCTCTCGGAGGCCGAGGAGGCGTCGCACGATCGATGATGAGTCGCTGTCCA	1507		
Qy	108	GCTCGGGCGCGCCG	120		
Db	1506	GCTCGGCTGCGG	1494		

```
RESULT 11
US-09-860-846-40
; Sequence 40, Application US/09860846
; Patent No. US20020164742A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/860,846
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-860-846-40

Query Match          20.0%; Score 30.8; DB 9; Length 2787;
Best Local Similarity 57.1%; Pred. No. 3.3;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 57 CGCTATCGTCGAGTCGGCGCGCGGACTCGACGATGACGAGATGACGAGTCGCGGCC 116
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 CGCTCTTACTGCTCGTCGGGACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 136
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 117 GCCGACTCGACGATGACGAGATGACGAGTCGCGGCCG 154
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 137 GCCGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 174
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-09-860-846-40/c
; Sequence 40, Application US/09860846
; Patent No. US20020164742A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/860,846
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-860-846-40

Query Match          20.0%; Score 30.8; DB 9; Length 2787;
Best Local Similarity 57.1%; Pred. No. 3.3;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CGCGCGAGTCGTCTCGTCATCGTCGAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCT 60
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 174 CGACAGACGGGGGTCTCCCGCTCGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 115
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 CATCGTCGAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 98
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 114 CTTCCCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 77
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 13
US-09-861-289-40
; Sequence 40, Application US/09861289
; Patent No. US20020110897A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/861,289
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-40

Query Match          20.0%; Score 30.8; DB 10; Length 2787;
Best Local Similarity 57.1%; Pred. No. 3.3;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 57 CGCTATCGTCGAGTCGGCGCGCGGACTCGACGATGACGAGATGACGAGTCGCGGCC 116
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 CGCTCTTACTGCTCGTCGGGACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 136
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 117 GCCGACTCGACGATGACGAGATGACGAGTCGCGGCCG 154
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 137 GCCGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 174
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-861-289-40/c
; Sequence 40, Application US/09861289
; Patent No. US20020110897A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/861,289
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-40

Query Match          20.0%; Score 30.8; DB 10; Length 2787;
Best Local Similarity 57.1%; Pred. No. 3.3;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CGCGCGAGTCGTCTCGTCATCGTCGAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCT 60
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 174 CGACAGACGGGGGTCTCCCGCTCGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 115
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 CATCGTCGAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 98
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 114 CTTCCCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 77
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```


GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 05:22:26 ; Search time 3509 Seconds
(without alignments)
1103.432 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggcggagctggtcatctc.....gagatgaccagctccggccg 154

Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues
Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	154	100.0	154	33	US-09-887-194A-13
2	154	100.0	154	33	US-09-887-194A-13
3	154	100.0	154	35	US-09-934-900-25
4	154	100.0	154	35	US-09-934-900-25
5	154	100.0	154	65	US-60-213-961-13
6	154	100.0	154	65	US-60-213-961-13
7	112	72.7	4974	34	US-09-906-209-17
8	112	72.7	4974	34	US-09-906-209-17
9	82.8	53.8	6611	35	US-09-934-900-26
10	82.8	53.8	6611	35	US-09-934-900-26
11	81	52.6	963	33	US-09-887-194A-29
12	81	52.6	963	33	US-09-887-194A-29
13	80	51.9	80	33	US-09-887-194A-12
14	80	51.9	80	33	US-09-887-194A-12
15	80	51.9	80	35	US-09-934-900-24
16	80	51.9	80	35	US-09-934-900-24
17	80	51.9	80	65	US-60-213-961-12
18	80	51.9	80	65	US-60-213-961-12
19	80	51.9	92	33	US-09-887-194A-14
20	80	51.9	92	33	US-09-887-194A-14
21	80	51.9	92	65	US-60-213-961-14
					Sequence 13, Appl
					Sequence 13, Appl
					Sequence 25, Appl
					Sequence 25, Appl
					Sequence 13, Appl
					Sequence 13, Appl
					Sequence 17, Appl
					Sequence 17, Appl
					Sequence 26, Appl
					Sequence 29, Appl
					Sequence 29, Appl
					Sequence 12, Appl
					Sequence 12, Appl
					Sequence 14, Appl
					Sequence 14, Appl

Db 1 CGCCGGAGCTGTCATCTCGCTCATCTGCTAGTCGGCGCCGGAGCTGGTCTATCTCGCT 60
QY 61 CATCGTCAGTTCGGCGCCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 120
Db 61 CATCGTCAGTTCGGCGCCGCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 120
QY 121 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 154
Db 121 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 154

RESULT 4
US-09-934-900-25/c
; Sequence 25, Application US/09934900
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BBI476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKSI33
US-09-934-900-25

Query Match 100.0%; Score 154; DB 35; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.7e-25;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCGGAGCTGTCATCTCGCTCATCTGCTAGTCGGCGCCGGAGCTGGTCTATCTCGCT 60
Db 154 CGCCGGAGCTGTCATCTCGCTCATCTGCTAGTCGGCGCCGGAGCTGGTCTATCTCGCT 95
QY 61 CATCGTCAGTTCGGCGCCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 120
Db 94 CATCGTCAGTTCGGCGCCGCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 35
QY 121 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 154
Db 34 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 1

RESULT 5
US-60-213-961-13
; Sequence 13, Application US/60213961
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BBI449 US PRV
; CURRENT APPLICATION NUMBER: US/60/213,961
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementa
; OTHER INFORMATION: region of pKSI33
US-60-213-961-13

Query Match 100.0%; Score 154; DB 65; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.7e-25;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCGGAGCTGTCATCTCGCTCATCTGCTAGTCGGCGCCGGAGCTGGTCTATCTCGCT 60
Db 1 CGCCGGAGCTGTCATCTCGCTCATCTGCTAGTCGGCGCCGGAGCTGGTCTATCTCGCT 60
QY 61 CATCGTCAGTTCGGCGCCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 120
Db 61 CATCGTCAGTTCGGCGCCGCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 120
QY 121 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 154
Db 121 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 154

RESULT 6
US-60-213-961-13/c
; Sequence 13, Application US/60213961
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXP
; FILE REFERENCE: BBI449 US PRV
; CURRENT APPLICATION NUMBER: US/60/213,961
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementa
; OTHER INFORMATION: region of pKSI33
US-60-213-961-13

Query Match 100.0%; Score 154; DB 65; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.7e-25;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCGGAGCTGTCATCTCGCTCATCTGCTAGTCGGCGCCGGAGCTGGTCTATCTCGCT 60
Db 154 CGCCGGAGCTGTCATCTCGCTCATCTGCTAGTCGGCGCCGGAGCTGGTCTATCTCGCT 95
QY 61 CATCGTCAGTTCGGCGCCGCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 120
Db 94 CATCGTCAGTTCGGCGCCGCGCGCGACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 35
QY 121 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 154
Db 34 ACTCGAGATGAGGAGATGACACGAGCTCCGCGCCG 1

RESULT 7
US-09-906-209-17
; Sequence 17, Application US/09906209
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; APPLICANT: Carlson, Tom

; APPLICANT: Ilag, Lawrence L.
; TITLE OF INVENTION: Plasmidic Phosphoglucomutase Genes
; FILE REFERENCE: BB1451 NA
; CURRENT APPLICATION NUMBER: US/09/906,209
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,712
; PRIOR FILING DATE: JULY 17, 2000
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 4974
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

Query Match 72.7%; Score 112; DB 34; Length 4974;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCGGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGCGGAGCTGGTCATCTCGCT 60
Db 4863 CGGCGGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGCGGAGCTGGTCATCTCGCT 4922
Qy 61 CATGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCC 112
Db 4923 CATGTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCC 4974

RESULT 8

US-09-906-209-17/c
; Sequence 17, Application US/09906209
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; APPLICANT: Carlson, Tom
; APPLICANT: Ilag, Lawrence L.
; TITLE OF INVENTION: Plasmidic Phosphoglucomutase Genes
; FILE REFERENCE: BB1451 NA
; CURRENT APPLICATION NUMBER: US/09/906,209
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,712
; PRIOR FILING DATE: JULY 17, 2000
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 4974
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

Query Match 72.7%; Score 112; DB 34; Length 4974;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 43 GGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGAT 102
Db 4974 GGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGAT 4915
Qy 103 GACGAGCTCGGCGCGGAGCTCGAGATGAGCGAGATGACGAGCTCGGCGG 154
Db 4914 GACGAGCTCGGCGCGGAGCTCGAGATGAGCGAGATGACGAGCTCGGCGG 4863

RESULT 9

US-09-934-900-26

; Sequence 26, Application US/09934900
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stea
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 6611
; TYPE: DNA
; ORGANISM: Plasmid pBS68
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (4436)...(4436)
; OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

Query Match 53.8%; Score 82.8; DB 35; Length 6611;
Best Local Similarity 97.7%; Pred. No. 3.8e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGCGGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGGTCATCTCGCT 60
Db 5348 CGGCGGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGGTCATCTCGCT 5407
Qy 61 CATGTCGAGTCGGCGCGCGGAGCT 86
Db 5408 CATGTCGAGTCGGCGCGGAGCT 5433

RESULT 10

US-09-934-900-26/c
; Sequence 26, Application US/09934900
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stea
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 6611
; TYPE: DNA
; ORGANISM: Plasmid pBS68
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (4436)...(4436)
; OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

Query Match 53.8%; Score 82.8; DB 35; Length 6611;
Best Local Similarity 97.7%; Pred. No. 3.8e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 69 AGTCGGCGGCGGAGCTCGACGATGAGCGAGATGACGAGCTCGGCGGAGCTCGACG 128
Db 5408 CATGTCGAGTCGGCGCGGAGCT 5433

Db 5433 ACTACGCCGCCGCGGACTCGACGATGAGCGAGATGACGAGTCCGCGCCGCGGCGGACTCGAGC 5374

QY 129 ATGAGCGAGATGACGAGTCCGCGCG 154

Db 5373 ATGAGCGAGATGACGAGTCCGCGCG 5348

RESULT 11

US-09-887-194A-29

; Sequence 29, Application US/09887194A

; GENERAL INFORMATION:

; APPLICANT: Glassman, Kimberly F.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Kinney, Anthony

; APPLICANT: Lowe, Keith S.

; APPLICANT: Nichols, Scott E.

; APPLICANT: Stecca, Kevin L.

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION

; FILE REFERENCE: BB1449 US NA

; CURRENT APPLICATION NUMBER: US/09/887,194A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 29

; LENGTH: 963

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary

; OTHER INFORMATION: region of pKS149

US-09-887-194A-29

Query Match

Best Local Similarity 52.6%; Score 81; DB 33; Length 963;

Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GCGGCGCGGCGGACTCGAGATGAGCGAGATGACGAGTCCGCGCCGCGGCGGACTCGAGATGAG 133

Db 883 GCGGCGCGGCGGACTCGAGATGAGCGAGATGACGAGTCCGCGCCGCGGCGGACTCGAGATGAG 942

QY 134 CGAGATGACGAGTCCGCGCG 154

Db 943 CGAGATGACGAGTCCGCGCG 963

RESULT 12

US-09-887-194A-29/c

; Sequence 29, Application US/09887194A

; GENERAL INFORMATION:

; APPLICANT: Glassman, Kimberly F.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Kinney, Anthony

; APPLICANT: Lowe, Keith S.

; APPLICANT: Nichols, Scott E.

; APPLICANT: Stecca, Kevin L.

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION

; FILE REFERENCE: BB1449 US NA

; CURRENT APPLICATION NUMBER: US/09/887,194A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 29

; LENGTH: 963

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary

; OTHER INFORMATION: region of pKS149

US-09-887-194A-29

Query Match

Best Local Similarity 52.6%; Score 81; DB 33; Length 963;

Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGCGGAGCTGTCATCTCGTCTCATGTCGAGTTCGGCGCGCGGAGCTGTCATCTCGCT 60

Db 963 CGCCGCGGAGCTGTCATCTCGTCTCATGTCGAGTTCGGCGCGCGGAGCTGTCATCTCGCT 904

QY 61 CATCTCGAGTCCGCGCGCG 81

Db 903 CATCTCGAGTCCGCGCGCG 883

RESULT 13

US-09-887-194A-12

; Sequence 12, Application US/09887194A

; GENERAL INFORMATION:

; APPLICANT: Glassman, Kimberly F.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Kinney, Anthony

; APPLICANT: Lowe, Keith S.

; APPLICANT: Nichols, Scott E.

; APPLICANT: Stecca, Kevin L.

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRE

; FILE REFERENCE: BB1449 US NA

; CURRENT APPLICATION NUMBER: US/09/887,194A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 12

; LENGTH: 80

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementa

; OTHER INFORMATION: region of pKS106 and pKS124

US-09-887-194A-12

Query Match

Best Local Similarity 51.9%; Score 80; DB 33; Length 80;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGCCGCGGAGCTGTCATCTCGTCTCATGTCGAGTTCGGCGCGCGGAGCTGTCATCTCGCTGATGAGC 97

Db 1 CGCCGCGGAGCTGTCATCTCGTCTCATGTCGAGTTCGGCGCGCGGAGCTGTCATCTCGCTGATGAGC 60

QY 98 GAGATGACGAGTCCGCGCG 117

Db 61 GAGATGACGAGTCCGCGCG 80

RESULT 14

US-09-887-194A-12/c

; Sequence 12, Application US/09887194A

; GENERAL INFORMATION:

; APPLICANT: Glassman, Kimberly F.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Kinney, Anthony

; APPLICANT: Lowe, Keith S.

; APPLICANT: Nichols, Scott E.

; APPLICANT: Stecca, Kevin L.

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRE

; FILE REFERENCE: BB1449 US NA

; CURRENT APPLICATION NUMBER: US/09/887,194A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 12

; LENGTH: 80

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementa

; OTHER INFORMATION: region of pKS106 and pKS124

US-09-887-194A-12

Query Match 51.9%; Score 80; DB 33; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGGTCACTCGCTCATCGTGGCGGCCGCCGACTCGACGATGAGC 97
|||||
Db 80 CGGCCGAGCTGGTCACTCGCTCATCGTGGCGGCCGCCGACTCGACGATGAGC 21
|||||
QY 98 GAGATGACCAAGCTCCGGCCG 117
|||||
Db 20 GAGATGACCAAGCTCCGGCCG 1

RESULT 15

US-09-934-900-24
; Sequence 24, Application US/09934900
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pK5106 and pK5124
US-09-934-900-24

Query Match 51.9%; Score 80; DB 35; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGGTCACTCGCTCATCGTGGCGGCCGCCGACTCGACGATGAGC 97
|||||
Db 1 CGGCCGAGCTGGTCACTCGCTCATCGTGGCGGCCGCCGACTCGACGATGAGC 60
|||||
QY 98 GAGATGACCAAGCTCCGGCCG 117
|||||
Db 61 GAGATGACCAAGCTCCGGCCG 80

Search completed: November 19, 2002, 06:28:11
Job time : 3552 secs

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	34.8	22.6	1681	6	US-10-271-889-7	Sequence 7, Appl	
2	34.8	22.6	1681	6	US-10-271-889-7	Sequence 7, Appl	
3	33	21.4	345	5	US-09-513-999C-8640	Sequence 8640, Ap	
4	33	21.4	345	5	US-09-513-999C-8640	Sequence 8640, Ap	
5	31.4	20.4	1707	6	US-10-267-255-68	Sequence 68, Appl	
6	31.4	20.4	1707	6	US-10-267-255-68	Sequence 68, Appl	
7	31.4	20.4	53500	6	US-10-267-255-76	Sequence 76, Appl	
8	31.4	20.4	53500	6	US-10-267-255-76	Sequence 76, Appl	
9	30.8	20.0	2787	6	US-10-271-889-40	Sequence 40, Appl	
10	30.8	20.0	2787	6	US-10-271-889-40	Sequence 40, Appl	
11	28.4	18.4	3284	6	US-10-240-425-1526	Sequence 1526, Ap	
12	28.4	18.4	3284	6	US-10-240-425-1526	Sequence 1526, Ap	
13	28.4	18.4	11220	6	US-10-271-889-32	Sequence 32, Appl	
14	28.4	18.4	11220	6	US-10-271-889-32	Sequence 32, Appl	
15	28.4	18.4	36778	6	US-10-271-889-48	Sequence 48, Appl	
16	28.4	18.4	36778	6	US-10-271-889-48	Sequence 48, Appl	
17	27.4	17.8	1030	6	US-10-240-425-1427	Sequence 1427, Ap	
18	27.4	17.8	1030	6	US-10-240-425-1427	Sequence 1427, Ap	
19	27.4	17.8	1419	6	US-10-267-255-61	Sequence 61, Appl	
20	27.4	17.8	1419	6	US-10-267-255-61	Sequence 61, Appl	
21	27.4	17.8	2327	1	PCT-US02-33723-66	Sequence 66, Appl	
22	27.4	17.8	2327	1	PCT-US02-33723-66	Sequence 66, Appl	
23	27.2	17.7	658	6	US-10-209-582-181	Sequence 181, App	
24	27.2	17.7	658	6	US-10-209-582-181	Sequence 181, App	
25	27.2	17.7	795	6	US-10-267-255-57	Sequence 57, Appl	
26	27.2	17.7	795	6	US-10-267-255-57	Sequence 57, Appl	

```

RESULT 3
US-09-513-999C-8640
; Sequence 8640, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8640
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 73
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 319
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 320
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 321
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 336
; OTHER INFORMATION: k=g or t
; FEATURE:

```

Qy	76	GGCCGCCGACTGACAGATGAGCGAGATGACAGCTCGGCCGCCGACTGACAGATGAGCG	135
Db <td>322</td> <td>GRMRTAGGCTGGGTGCTGAGGGAAGGACCACTCGGCGCGTAGCTGGTGGTGAGAG</td> <td>263</td>	322	GRMRTAGGCTGGGTGCTGAGGGAAGGACCACTCGGCGCGTAGCTGGTGGTGAGAG	263
Qy <td>136</td> <td>AGATGACCAGCTCCGCC</td> <td>152</td>	136	AGATGACCAGCTCCGCC	152


```
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 36778
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-10-271-889-48

Query Match      18.4%; Score 28.4; DB 6; Length 36778;
Best Local Similarity 52.5%; Pred. No. 23;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Oy 37 GCGGCGGAGCTGTCATCTCGTCATGTCGAGTCGCGCGGCCGCGACTCGACGATCAG 96
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26247 GCTGGCGCCGCTGCTCAGCGGGCTCACCGGGGATCGGGGTCGGCGCGCGGTCAA 26306

Oy 97 CGAGATGACCACTCCGCGCCCGCGACTCGAGGATGCGGATGACCACTCCGCGCG 154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26307 CCAGCGGAGGCGCGCGCGGAGGCGGCGGAGGCGGACACGACCTCGCGCGCGG 26364
```

Search completed: November 19, 2002, 05:29:53
Job time : 194 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 05:26:44 ; Search time 2117 Seconds
(without alignments)
1178.132 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggcgagagctgctatctc.....gagatgaccagctccggcg 154

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16134066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthba:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.6	23.8	175	12	BF945949
2	36.6	23.8	175	12	BF945949
3	36.2	23.5	627	17	CNS030BV
4	36.2	23.5	627	17	CNS030BV
5	36.2	23.5	787	17	A2933792
6	36.2	23.5	787	17	A2933792

7	36.2	23.5	1057	17	CNS03W2P
8	36.2	23.5	1057	17	CNS03W2P
9	36	23.4	972	17	CNS04TDK
10	36	23.4	972	17	CNS04TDK
11	35.6	23.2	367	14	BQ767987
12	35.8	23.2	367	14	BQ767987
13	35.4	23.0	590	9	AI399069
14	35.4	23.0	590	9	AI399069
15	35	22.7	441	12	BF483067
16	35	22.7	441	12	BF483067
17	35	22.7	571	14	BQ805125
18	35	22.7	571	14	BQ805125
19	34.8	22.6	430	12	BG279219
20	34.8	22.6	430	12	BG279219
21	34.8	22.6	497	9	AL829848
22	34.8	22.6	497	9	AL829848
23	34.8	22.6	558	9	AI397686
24	34.8	22.6	558	9	AI397686
25	34.8	22.6	673	14	BQ841269
26	34.8	22.6	673	14	BQ841269
27	34.6	22.5	1012	17	CNS03D7T
28	34.6	22.5	1012	17	CNS03D7T
29	34.4	22.3	415	12	BF462402
30	34.4	22.3	415	12	BF462402
31	34.4	22.3	503	12	BF466956
32	34.4	22.3	503	12	BF466956
33	34.4	22.3	769	17	BH555985
34	34.4	22.3	769	17	BH555985
35	34.4	22.3	771	17	BH447921
36	34.4	22.3	771	17	BH447921
37	34.2	22.2	288	14	BQ756129
38	34.2	22.2	288	14	BQ756129
39	34.2	22.2	500	12	BG366731
40	34.2	22.2	500	12	BG366731
41	34.2	22.2	551	14	BQ464534
42	34.2	22.2	551	14	BQ464534
43	34.2	22.2	647	13	BI960178
44	34.2	22.2	647	13	BI960178
45	34.2	22.2	669	9	AU078265

ALIGNMENTS

RESULT 1	BF945949	175 bp	mRNA	linear	EST 22-JAN-2001
LOCUS	CM0-NN1155-271000-628-a09	NN1155	Homo sapiens	cdna	mRNA sequence.
DEFINITION	BF945949				
ACCESSION	BF945949				
VERSION	BF945949.1	GI:12363224			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 175)				
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	PROC. Natl. Acad. Sci. U.S.A.	97 (7)			3491-3496 (2000)
MEDLINE	20202663				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001				

genome. For more information, please take a look at

	Matches	50;	Conservative	0;	Mismatches	23;	Indels	0;	Gaps	0;
Qy	28	GTCCAGTCGGGGCGGAGCTGCTCATCTCGATCGGGGGCCGCCGACTC	87							
		TTT								
Db	570	GTCCGGAGCCGGGGCGGCTCTGCTGTCTCGCGCTCTCCGAGACGCTCTCCGCCGAGA	511							
Qy	88	GACGATGAGCGAG	100							
Db	510	GACCATGAGCGAG	498							

RESULT 9	
CNS04TDC	
LOCUS	972 bp DNA linear GSS 24-MAY-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence T3 end of clone 013112 of library A from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL306353
VERSION	AL306353.1 GI:8204690
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetraodon nigroviridis.
ORGANISM	Tetraodon nigroviridis. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

RODRIGUES
Roest-Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Barnot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.

TITLE
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL
REFERENCE
Unpublished
2 (bases 1 to 972)

AUTHORS
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fiamas, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon lineolatus

JOURNAL
REFERENCE
Unpublished
3 (bases 1 to 972)
freshwater purerfish tetraodon nigroviridis

REFERENCE	AUTHORS	TITLE
3 (Pages 1 to 972)	Genoscope.	Direct Submission

JOURNAL COMMENT
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/mammals/tetraodon>

FEATURES	Location/Qualifiers	source
	1..972	

```

source
1.912
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"

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/dev/zero | dd count=99003  
of_clone="013112"  
/clone_lib="A"
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BASE COUNT      233 a      254 c      267 g      152 t
                /note="Genoscope sequence ID : C1AA003ZE01A1-end : T3"
                66 others

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ORIGIN	Query Match	23 48	Score 35	DB 17	Length 972

Query Match	23.4%	Score 36;	DB 17;	Length 972;
Best Local Similarity	60.0%	Pred. No. 64;		
Matches	57;	Conservative	0;	Mismatches 38.
				Index's 0.

	Matches	J;	Conservative	Mismatches	Indels	Gaps
QY	55	CRGGCTATCGTTCGGTGGGGCCGCCACTCGACGATGACGGAGATGACCAAGTCCGG	0;	0;	38;	0;

db

474 CTCGCTCATGGTCTCGTCGGCGSAGGACGTCTCGACAGCGCNAGACAGCANAGCGG 533

QY 115 CGCCCGACTCGACGATGAGCGAGATGACCAGCTCC 149

Db 534 CCGGCTCCGGACATCGTCCGACCCNAGGAGACC 568

RESULT 10

RESULT 10
CNS04TDK/C

LOCUS	CNS04TDK	972 bp	DNA	linear	GSS 24-MAY-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence T3 end of clone 03112 of library A from Tetraodon nigroviridis, genomic survey sequence.				
ACCESSION	AL306353				
VERSION	AL306353.1	GI:8204690			
KEYWORDS	GSS: genome survey sequence.				
SOURCE	Tetraodon nigroviridis.				
ORGANISM	Tetraodon nigroviridis.				

REFERENCE
AUTHORS
1 (bases 1 to 972)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL
Unpublished
REFERENCE
AUTHORS
2 (bases 1 to 972)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE
Characterization and repeat analysis of the compact genome of the freshwater euryfish Tetraodon lineatus

REFERENCE	3 (bases 1 to 972)
AUTHORS	Genoscope.
TITLE	Direct Submission

JOURNAL	Submitted (12-APR-2000)
TITLE	Direct Submission
COMMENT	This sequence is a single read and was generated as part of a large

COMMENT
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

genome. For more information, please take a look at
 . <http://www.genoscope.cns.fr/Tetraodon>.
 Location/Qualifiers

```
source
1. .972
/organism="Tetraodon nigroviridis"
```

```
/db_xref=taxon:99883"
/clone="013112"
/clone_lib="2"

```

```

BASE COUNT
233 a 254 C 267 a 152 t
/clone_lib="A"
/note="Genoscope sequence ID : C1AA003ZE01A1-end : T3"
66 Others

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ORIGIN	233 d	234 C	267 g	152 L	66 others
BASE COUNT					

Query Match	23.4%	Score 36;	DB 17;	Length 972;
Best Local Similarity	60.0%	Pred. No. 64;		

```

Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```

6 GGAGCTGGTCACTCTCGCTCATCTCGAGTCGGCGGAGCTGGTCACTCTCGCTCATCG 65

568 GCGTCTCTCTTCCGCTTCCGAGTATCTCGGCGGAGCTGGTCACTCTCGCTCATCG 508

DB 568 GGTTCCTCTTNGGGTCGACGATGTCGGGGAGCCGGCGCGCTTTCCTGTTCTNGCGCCTGT 509

Ov 66 TCGACTCGGGGCGCGGCGACTCGACGATGAGCGAG 100

QY 66 TCGAGTCGGGGGCGGACATCGAGATGAGCGGAG 100
||||| ||| |||||||| ||| |||||||||
Db 508 CCGAGACGTCCTCCGCCGACGAGACCATGAGCGGAG 474

[illegible]

RESULT 11
BQ767987
LOCUS

LOCUS	BQ767987	367 bp	mRNA	linear	EST 26-JUL-2002
DEFINITION	EBr08_S0010_K07_R root, 3 week, drought-stressed, cv Optic, EBr08				
	Hordeum vulgare cDNA clone EBr08_S0010_K07_5'				mRNA sequence

Hordeum vulgare cDNA clone EBro8_S0010_K07 5', mRNA sequence.

ACCESSION	BQ767987
VERSION	BQ767987.1
GI:	21976461

VERSION	EST.
KEYWORDS	Hordeum vulgare.
SOURCE	
EQ/0/987.1	GI:219/0301

ORGANISM

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 367)
AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 05:24:44 : Search time 2709 seconds
(without alignments)
1654.423 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cgccggagctggtcatctc.....gagatgaccagctccggccg 154

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl :

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_lm.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_jm.*
- 20: em_lm.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rdt.*
- 36: em_htg_mam.*
- 37: em_htg_vit.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	154	100.0	154	6	AX367128	Sequence
2	154	100.0	154	6	AX367128	Sequence
3	154	100.0	154	6	AX392336	Sequence
4	154	100.0	154	6	AX392336	Sequence
5	112	72.7	4974	6	AX353724	Sequence
6	112	72.7	4974	6	AX353724	Sequence
7	82.8	53.8	6611	6	AX392337	Sequence
8	82.8	53.8	6611	6	AX392337	Sequence
9	81	52.6	963	6	AX367144	Sequence
10	81	52.6	963	6	AX367144	Sequence
11	80	51.9	80	6	AX367127	Sequence
12	80	51.9	80	6	AX367127	Sequence
13	80	51.9	80	6	AX392335	Sequence
14	80	51.9	80	6	AX392335	Sequence
15	80	51.9	92	6	AX367129	Sequence
16	80	51.9	92	6	AX367129	Sequence
17	45.8	29.7	1717	6	AX367139	Sequence
18	45.8	29.7	1717	6	AX367139	Sequence
19	38.2	24.8	10348	1	AE004846	Pseudomon
20	38.2	24.8	10348	1	AE004846	Pseudomon
21	36.4	23.6	115036	2	AC107207	Oryza sat
22	36.4	23.6	115036	2	AC107207	Oryza sat
23	36.2	23.5	8973	1	AY081837	Bradyrhiz
24	36.2	23.5	8973	1	AY081837	Bradyrhiz
25	36.2	23.5	123169	9	AC008771	Homo sapi
26	36.2	23.5	123169	9	AC008771	Homo sapi
27	36.2	23.5	126054	9	AC018764	Homo sapi
28	36.2	23.5	126054	9	AC018764	Homo sapi
29	36	23.4	131603	2	AC097280	Oryza sat
30	36	23.4	131603	2	AC097280	Oryza sat
31	36	23.4	190050	1	AL646059	Ralstonia
32	36	23.4	190050	1	AL646059	Ralstonia
33	35.8	23.2	1102	8	HVMYB2	H. vulgare m
34	35.8	23.2	1102	8	HVMYB2	H. vulgare m
35	35.8	23.2	22115	1	SCC22	Streptomy
36	35.8	23.2	22115	1	SCC22	Streptomy
37	35.8	23.2	106161	2	AC120984	Oryza sat
38	35.8	23.2	106161	2	AC120984	Oryza sat
39	35.8	23.2	180186	8	AP003104	Oryza sat
40	35.8	23.2	180186	8	AP003104	Oryza sat
41	35.6	23.1	102529	2	AP004747	Oryza sat
42	35.6	23.1	102529	2	AP004747	Oryza sat
43	35.6	23.1	340900	1	SME591791	Sinorhizo
44	35.6	23.1	340900	1	SME591791	Sinorhizo
45	35	22.7	1020	9	AB078417	Homo sapi

ALIGNMENTS

RESULT 1	AX367128	AX367128	154 bp	DNA	linear	PAT 16-FEB-2002
LOCUS	Sequence 13 from Patent WO0200904.					
DEFINITION	AX367128					
ACCESSION	AX367128					
VERSION	AX367128.1	GI:18855329				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE	1					
AUTHORS	Glassman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.L. and Nichols, S.E.					
TITLE	Recombinant constructs and their use in reducing gene expression					
JOURNAL	Patent: WO 0200904-A 13 03-JAN-2002;					

E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
Location/Qualifiers
1. .154
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"
BASE COUNT 24 a 53 c 53 g 24 t
ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 60
Db 1 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 60

Qy 61 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 120
Db 61 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 120

Qy 121 ACTCGAGATGAGCGAGATGACGAGCTCCGGCG 154
Db 121 ACTCGAGATGAGCGAGATGACGAGCTCCGGCG 154

RESULT 2
AX367128/c
LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO020904.
ACCESSION AX367128
VERSION AX367128.1 GI:18855329
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 020904-A 13 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
Location/Qualifiers
1. .154
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"
BASE COUNT 24 a 53 c 53 g 24 t
ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 60
Db 154 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 95

Qy 61 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 120
Db 94 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 35

Qy 121 ACTCGAGATGAGCGAGATGACGAGCTCCGGCG 154
Db 34 ACTCGAGATGAGCGAGATGACGAGCTCCGGCG 1

RESULT 3
AX392336
LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)
Location/Qualifiers
1. .154
/organism="synthetic construct"
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/note="ELVISLIVES complementary region of pKS133"
BASE COUNT 24 a 53 c 53 g 24 t
ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 60
Db 154 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 95

Qy 61 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 120
Db 94 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 35

AX392336
AX392336.1 GI:19700689
synthetic construct.
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)
Location/Qualifiers
1. .154
/organism="synthetic construct"
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/note="ELVISLIVES complementary region of pKS133"
BASE COUNT 24 a 53 c 53 g 24 t
ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 60
Db 1 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 60

Qy 61 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 120
Db 61 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 120

Qy 121 ACTCGAGATGAGCGAGATGACGAGCTCCGGCG 154
Db 121 ACTCGAGATGAGCGAGATGACGAGCTCCGGCG 154

RESULT 4
AX392336/c
LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)
Location/Qualifiers
1. .154
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"
BASE COUNT 24 a 53 c 53 g 24 t
ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 60
Db 154 CGCGCGAGCTGGTTCATCTCGCTCATCTCGAGTCGCGCGCGGAGCTGGTTCATCTCGCT 95

Qy 61 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 120
Db 94 CATCTCGAGTCGGCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTCCGGCGCG 35

1. *Chlorophyll a* (Chl a) content was determined using a spectrophotometer (Shimadzu UV-1601) at 663 nm. The concentration of Chl a was calculated using the following formula: $\text{Chl a (mg/L)} = 12.7 \times \text{OD}_{663}$.

Db 5373 ATGAGCGAGATGACCGAGCTCCGGCCG 5348

RESULT 9
LOCUS AX367144
DEFINITION Sequence 29 from Patent WO0200904.
ACCESSION AX367144
VERSION AX367144.1 GI:18853345
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 29 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
Location/Qualifiers
1..963
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS149"
BASE COUNT 240 a 243 c 248 g 232 t
ORIGIN

Query Match 52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 GCGCGCGGACTCGACGATGACGAGATGACCGAGTCCGGCGCGACTCGACGATGAG 133
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Qy 134 CGAGATGACCGAGTCCGGCCG 154
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Db 943 CGAGATGACCGAGTCCGGCCG 963

RESULT 10
LOCUS AX367144/c
DEFINITION Sequence 29 from Patent WO0200904.
ACCESSION AX367144
VERSION AX367144.1 GI:18853345
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 29 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS149"
BASE COUNT 240 a 243 c 248 g 232 t
ORIGIN

Query Match 52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGCGCGGAGTGGTCTCGTCTCGTCTCGGCGCGGAGCTGGTCTCGTCTCGT 60
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Qy 61 CATCGTCGAGTCGGCGCGCG 81
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Db 903 CATCGTCGAGTCGGCGCGCG 883

RESULT 11
LOCUS AX367127
DEFINITION Sequence 12 from Patent WO0200904.
ACCESSION AX367127
VERSION AX367127.1 GI:18853328
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 12 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS106 and
PKS124"
BASE COUNT 12 a 28 c 28 g 12 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 38 CGCGCGGAGTGGTCTCGTCTCGTCTCGGCGCGCGCGCGCGCGCGATGAGC 97
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Db 1 CGCGCGGAGTGGTCTCGTCTCGTCTCGGCGCGCGCGCGCGCGCGATGAGC 60
Qy 98 GAGATGACCGAGTCCGGCCG 117
|||||
Db 61 GAGATGACCGAGTCCGGCCG 80

RESULT 12
LOCUS AX367127/c
DEFINITION Sequence 12 from Patent WO0200904.
ACCESSION AX367127
VERSION AX367127.1 GI:18853328
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 12 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
Location/Qualifiers
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/note="ELVISLIVES complementary region of PKS106 and
PKS124"
BASE COUNT 12 a 28 c 28 g 12 t
ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 6e-06;

RESULT 14							PAT 23-MAR-2002
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LOCUS		80 bp	DNA	linear			
DEFINITION	Sequence 24 from Patent WO0216565..						
ACCESSION	AX392335						
VERSION	AX392335.1 GI:19700688						
KEYWORDS	. synthetic construct.						
SOURCE	synthetic construct						
ORGANISM	artificial sequences.						
REFERENCE	1						
AUTHORS	Booth,J.R., Caboon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.						
TITLE	Nucleotide sequences of a new class of diverged delta-9 stearyl-ac desaturase genes						
JOURNAL	Patent: WO 0216565-A 24 28-FEB-2002;						
	E. I. du Pont de Nemours and Company (US)						
FEATURES	Location/Qualifiers						
source	1..80 /organism="synthetic construct" /db_xref="taxon:32630"						
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BASE COUNT	12 a 28 c 28 g 12 t						
ORIGIN							

Query Match	51.9%	Score 80;	DB 6;	Length 92;
Best Local Similarity	100.0%	Pred. No. 5.9e-06;		
Matches 80;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	7	CGGCGGAGCTGGTCATCTCGTCATCGTGAGTTCGGCGGCCGCGGACTCGACGATGAGC	66	
QY	98	GAGATGACCACTCCGGCCG	117	
Db	67	GAGATGACCACTCCGGCCG	86	

Search completed: November 19, 2002, 07:14:04
Job time : 2740 secs